

P&S Mobile Genomics

Lecture 10: Genome Assembly

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Agenda for Today

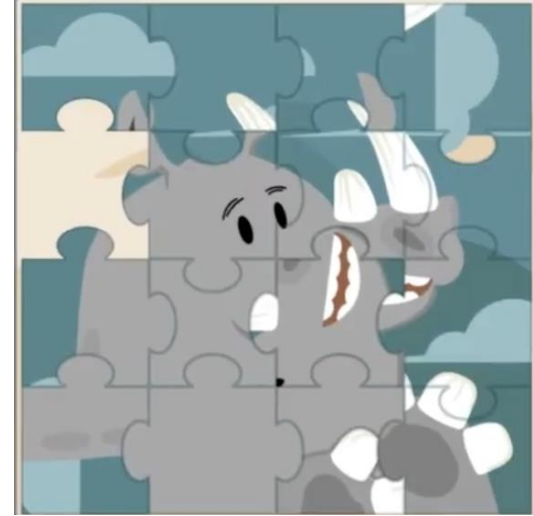
- Genome Assembly
 - Basics
 - Overlap-Layout-Consensus

Recall: Caveats of Sequencing Technologies

Small pieces of a puzzle
short reads (Illumina)



Large pieces of a puzzle
long reads (ONT & PacBio)



Which sequencing technology is the best?

☐ 100-300 bp

☐ low error rate ($\sim 0.1\%$)

☐ 500-2M bp

☐ high error rate ($\sim 15\%$)

<https://www.pacb.com/smrt-science/smrt-sequencing/hifi-reads-for-highly-accurate-long-read-sequencing/>

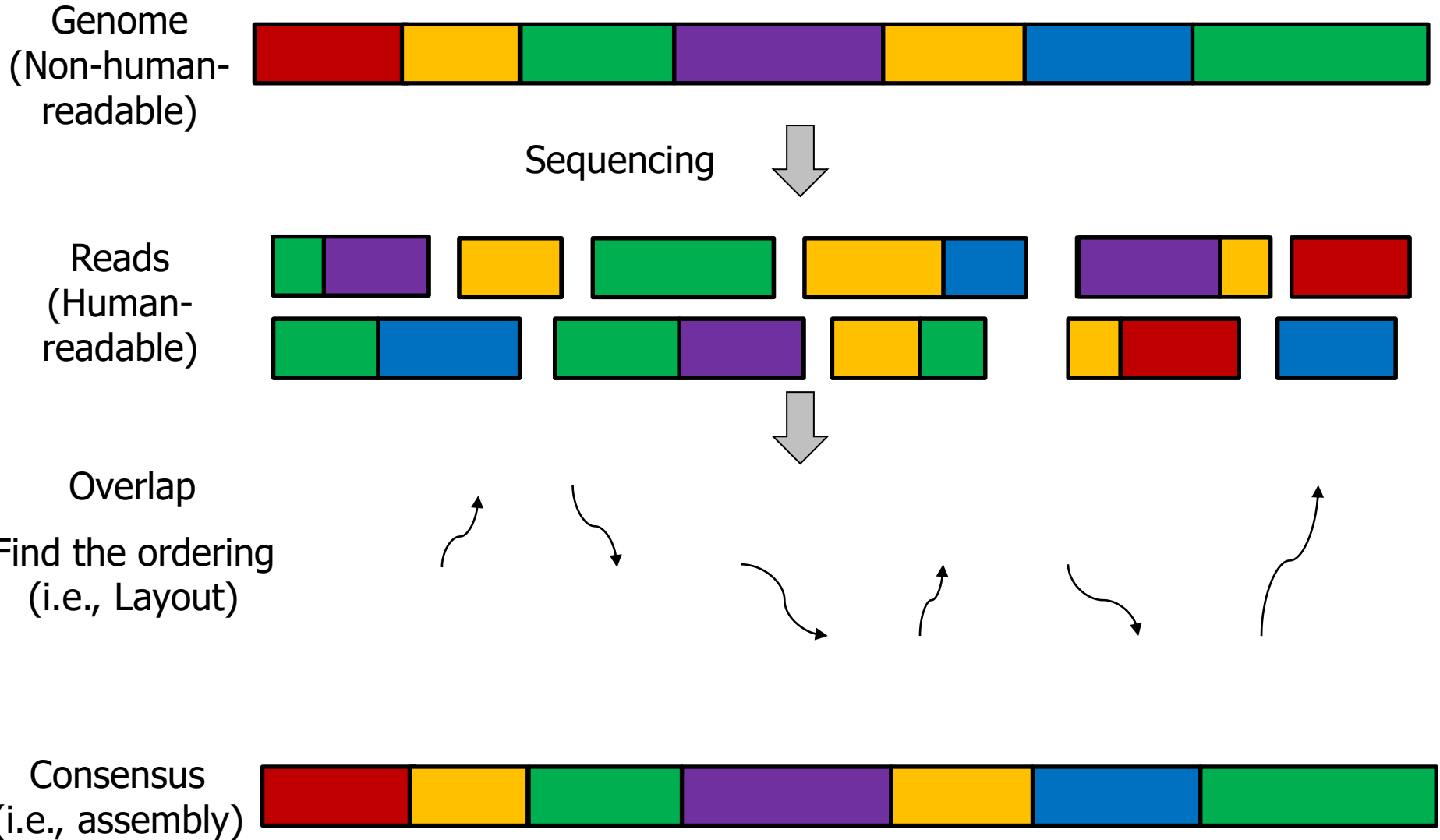
Recall: A Dream

Looking forward,
Will we be able to read
the entire genome sequence?

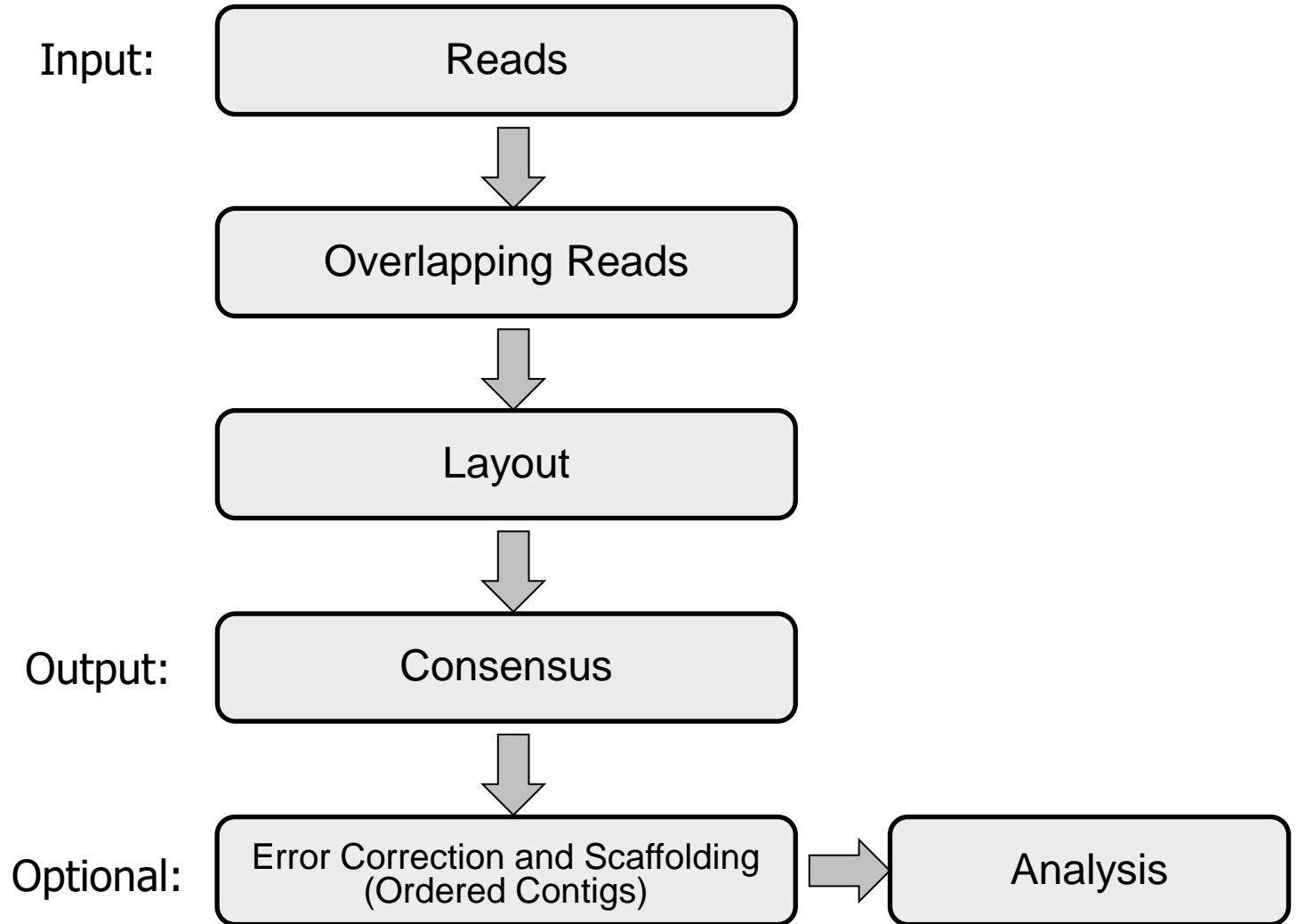
Genome Assembly Basics

- There is no sequencing technology that can read an entire chromosome from start to end
 - Rather we have short fragments of genome: **Reads**
- Reconstruct the actual genome from its pieces to
 - Compare two genomes to reveal large structural variations as well as small mutations to **pinpoint diseases** and **study certain phenotypes** (e.g., eye color, hair color)
 - Map known genes
 - Use it as a reference to map reads from the same species
 - ...
- Two major approaches to reconstruct a genome
 - Hierarchical sequencing
 - Human Genome Project
 - **Slow, expensive**, but **highly accurate and contiguous assembly**
 - Whole genome shotgun (WGS) sequencing
 - **Fast, cheaper**, but **less accurate and less contiguous**

Genome Assembly from WGS Sequencing



A Common Assembly Pipeline



Overlapping Reads

- Goal: Solve the genome assembly puzzle by filling the gaps with **overlapping reads**
- **Overlaps**: Matching blocks between **pairs of reads** using
 - Exact matching short subsequences between reads
 - Suffix Tree
 - Alignment
- **Condition**: Suffix of a read overlaps prefix of another read

ATTGAAGCACGTATACTA ●
AAGCACGTATACTATTACT ●
GCACGTGGACTATTACTAA ●
TACCGATTGGACTATCCATTAC ●
GGACTATCCATTACACCTGGAT ●
CATTTACACCTGGATGACTAC ●
ACGGATACCATACTTACT :
GGATCTTACTTACTGACTAC :
AGCGTTACGTCCTAGC .
GGTACCCCTGAGCCTAGAACT

Overlapping Reads:

ATTGAAGCACGTATACTA
| | | | | | | | | | | | | |
AAGCACGTATACTATTACT

ATTGAAGCACGTATACTA
| | | | | | | | | | | | | |
GCACGTGGACTATTACTAA

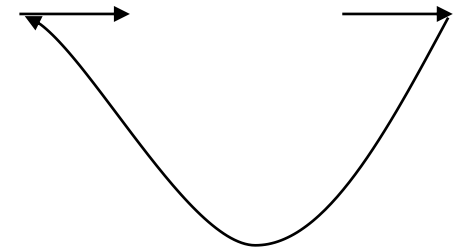
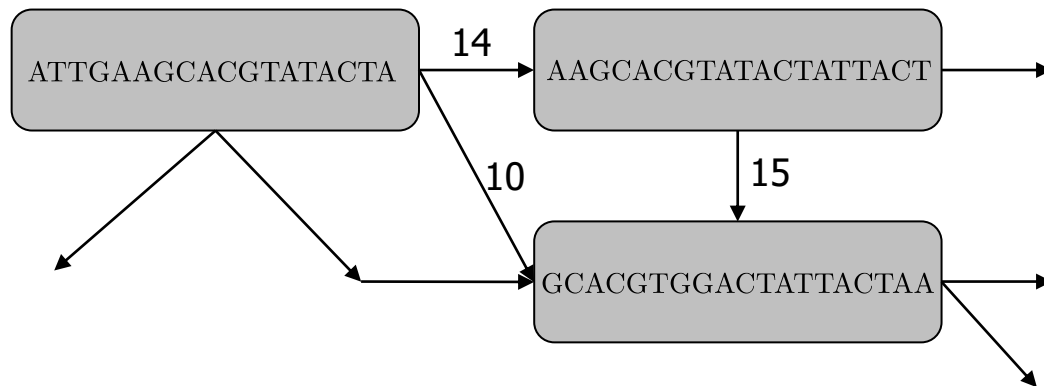
AAGCACGTATACTATTACT
| | | | | | | | | | | | | |
GCACGTGGACTATTACTAA

TACCGATTGGACTATCCATTAC
| | | | | | | | | | | | | |
GGACTATCCATTACACCTGGAT

Storing Overlaps in Graphs

- **Graphs** are useful to 1) avoid storing **redundant reads** and 2) identify **ordering of overlaps**
- **Nodes**: Reads/Chunks of reads
- **Directed Edges**: When **suffix of one read overlaps prefix of another read**
 - **Label**: Number of matches between overlapping reads

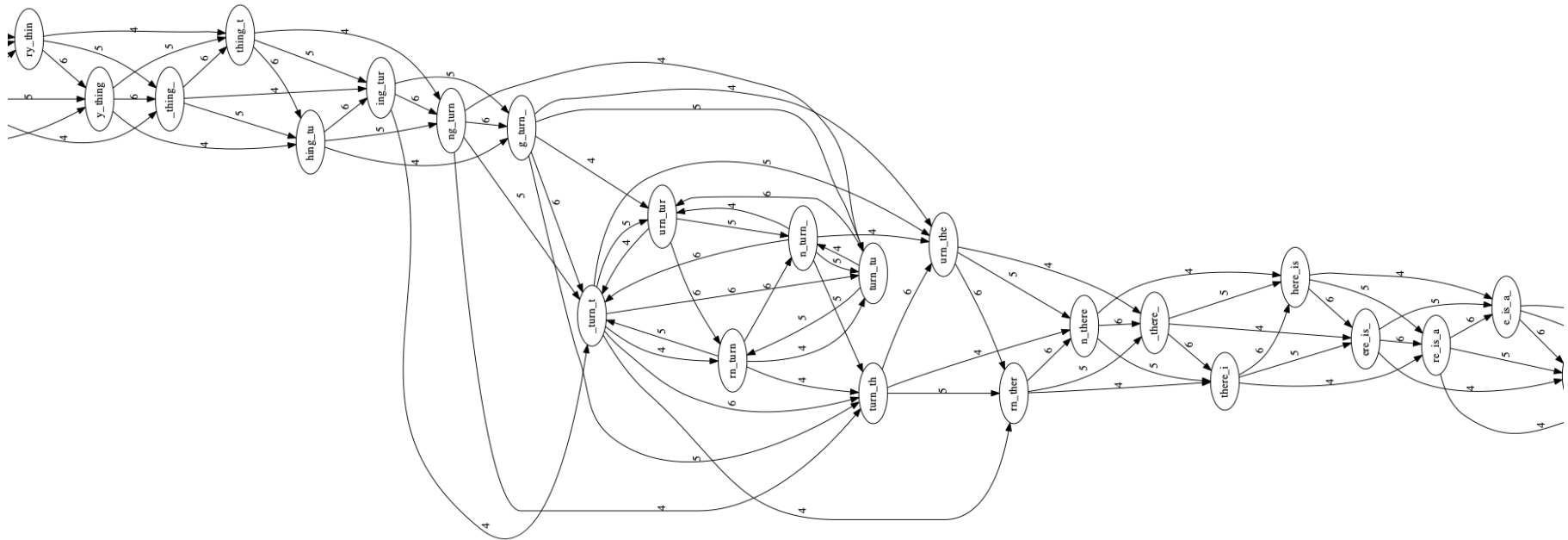
ATTGAAGCACGTATACTA	ATTGAAGCACGTATACTA	AAGCACGTATACTATTACT
14	10	10
AAGCACGTATACTATTACT	GCACGTGGACTACCT	GCACGTGGACTACCT



- **Edges can get quite messy**

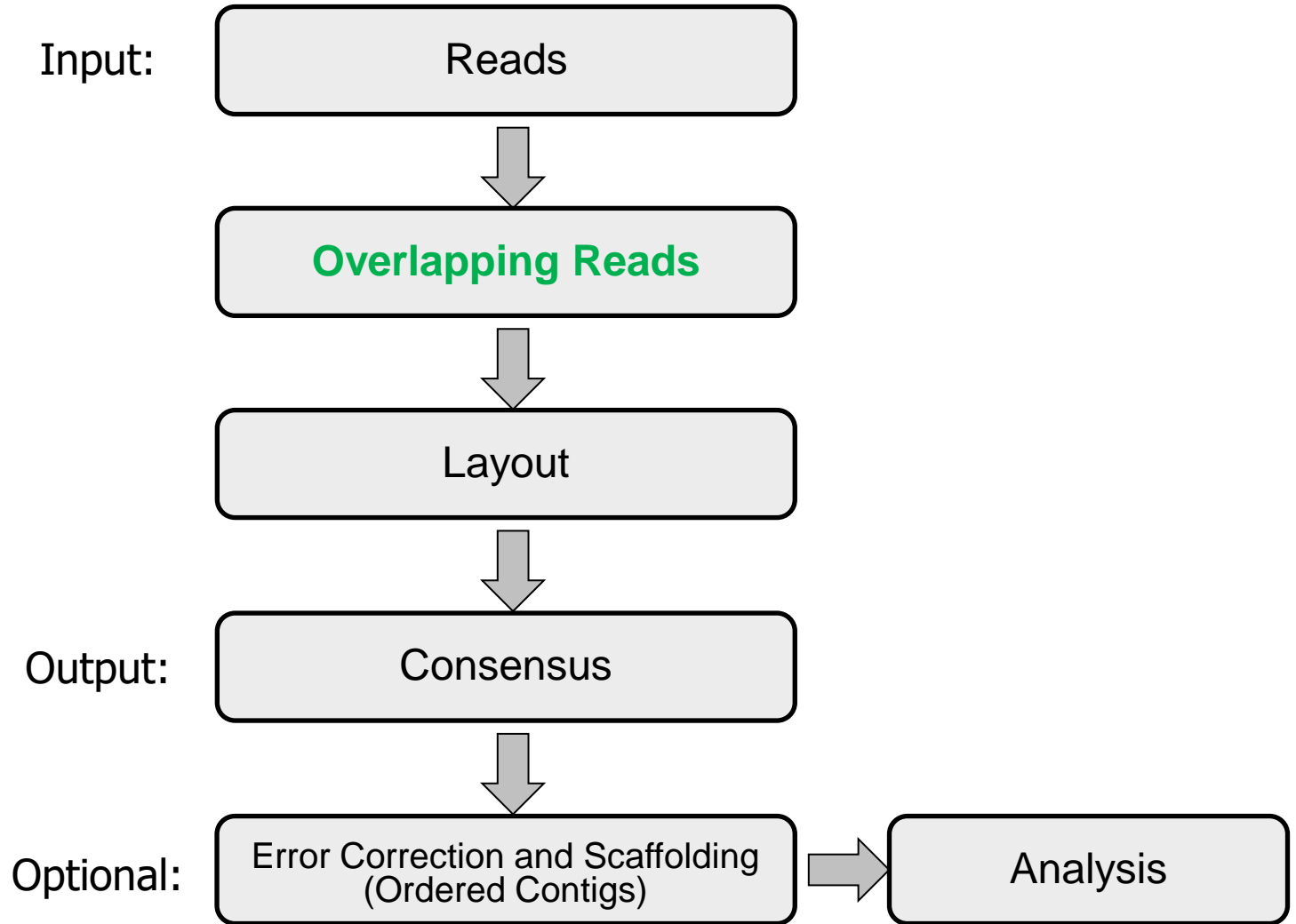
A Messy Overlap Graph

- Let's construct the following string from its **pieces**
 - to_every_turn_turn_turn_there_is_a_season
- **Pieces**: Every substrings of length 7 (7-mers)
- A part of such an overlap graph:



- **Goal:** Find assembly by **ordering overlaps** correctly
- How to find a **simpler** ordering of overlaps relative to each other from the overlap graph?

A Common Assembly Pipeline

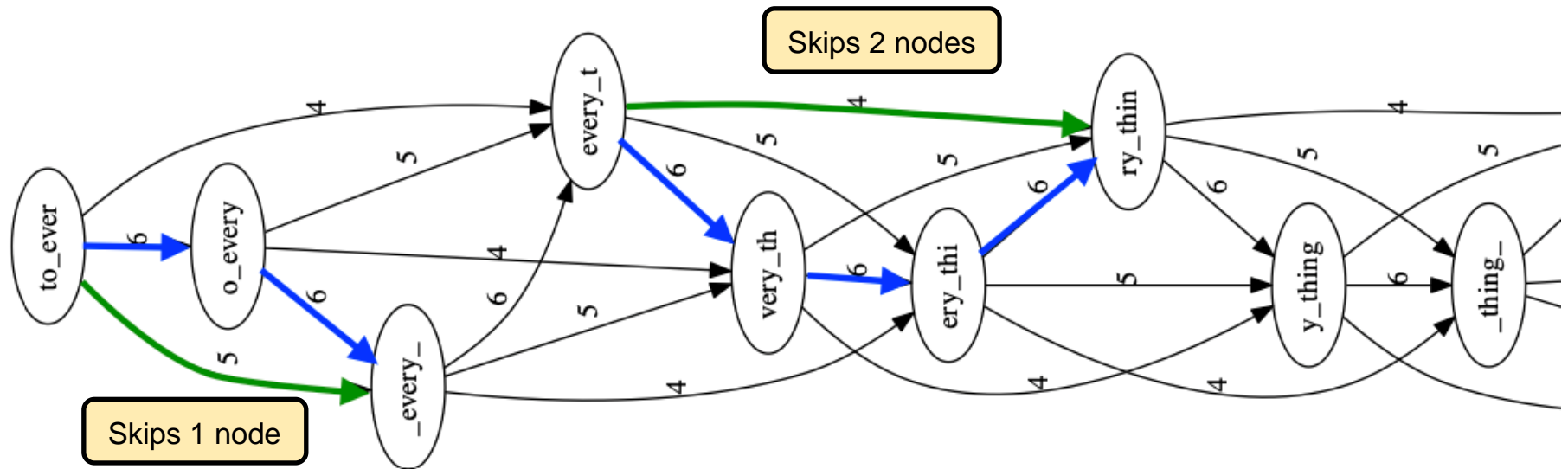


Layout – Graph Cleaning

- Overlap graphs may contain **redundant information**
 - **Transitive (redundant) edges:** An edge from node v to node w ($v \rightarrow w$) is transitive if:
 - There exists $v \rightarrow u$ and $u \rightarrow w$
 - We can remove the edge $v \rightarrow w$ without losing the ability to visit w starting from v
 - **Bubbles:** A directed acyclic graph with sink and source nodes v and w such that
 - There exist at least two *isolated* paths from v to w
 - We want to collapse bubbles to simplify the overlap graph
 - **Tips:** Short branches in the graph that terminate very early

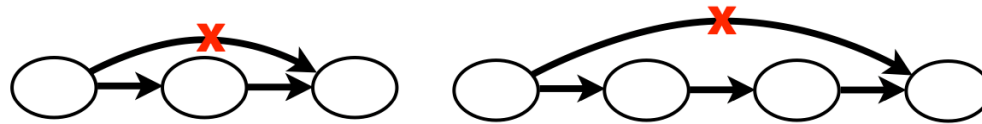
Layout – Transitive Reduction

- Overlap graphs may contain **redundant edges**
 - **Transitive edges** can be removed without losing the connectivity information of the graph
 - The **green edges** are **transitive edges** because **blue edges** provide the connectivity information that green edges provide

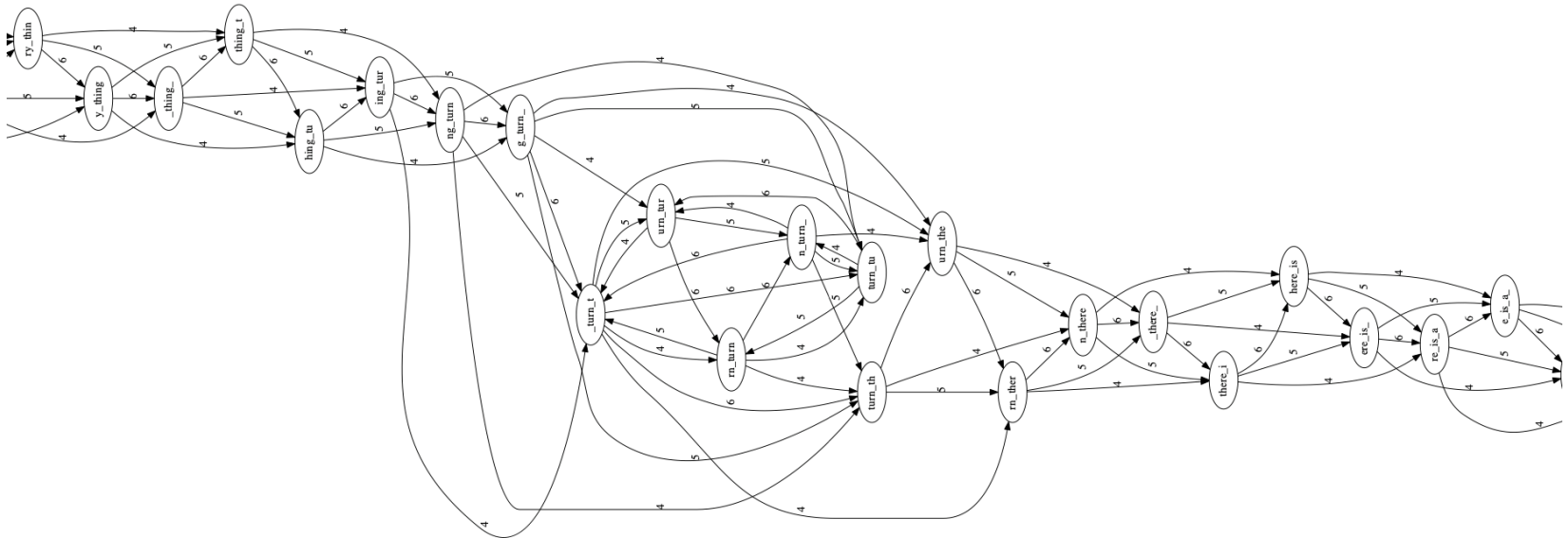


Layout – Transitive Reduction Example

- Overlap graphs may contain **redundant edges**
 - Transitive edges that can be removed without losing the connectivity information of the graph
 - Let's remove the transitive edges that skip one or two nodes:

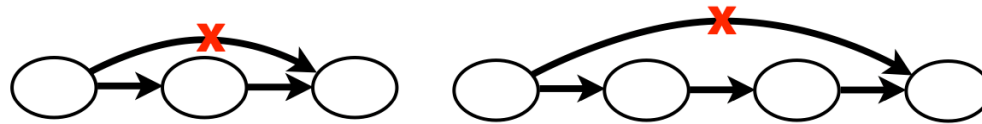


- Remember the messy overlap graph?

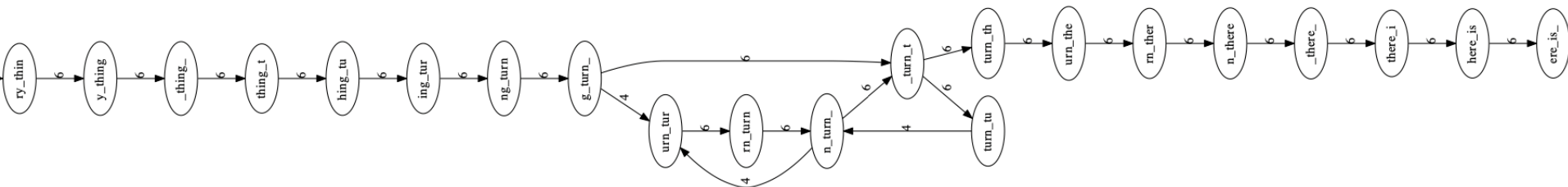


Layout – Transitive Reduction Example

- Overlap graphs may contain **redundant edges**
 - Transitive edges that can be removed without losing the connectivity information of the graph
 - Let's remove the transitive edges that skip one or two nodes:



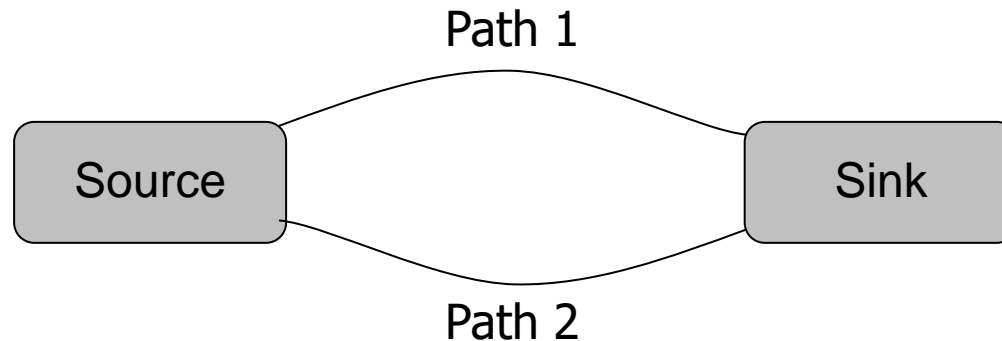
- After the transitive reduction:



- It is now much easier to identify **ordering of overlaps** from this graph

Layout – Bubble Collapsing (Popping)

- Bubbles: Different multiple paths with the same source and sink
 - May remain undetected after transitive edge removal
 - One of the paths are collapsed (e.g., the shorter one)
 - Shorter paths may be due to **repeats** after transitive reduction



- We can collapse bubbles to
 - Reduce the complexity of the overlap graph
 - Improve the contiguity of the assembly inferred from the graph
- Why do we have bubbles?
 - Sequencing errors (missing overlaps)
 - Variants between parent genomes (diploid and polyploid genomes)

Layout – Readings on Graph Cleaning

- Read the following paper if you are curious about
 - How the transitive reduction works:

BIOINFORMATICS

Vol. 21 Suppl. 2 2005, pages ii79–ii85
doi:10.1093/bioinformatics/bti1114

Genes and Genomes

The fragment assembly string graph

Eugene W. Myers

Department of Computer Science, University of California, Berkeley, CA, USA

- How to collapse bubbles in overlap graphs:

Minimap and miniasm: fast mapping and de novo assembly for noisy long sequences FREE

[Heng Li](#) [Author Notes](#)

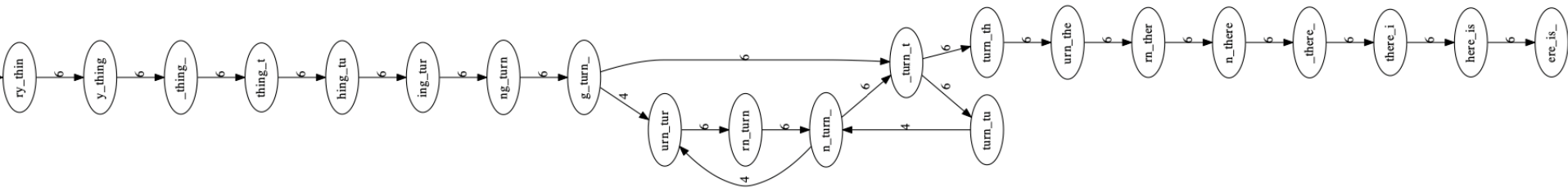
Bioinformatics, Volume 32, Issue 14, 15 July 2016, Pages 2103–2110,

<https://doi.org/10.1093/bioinformatics/btw152>

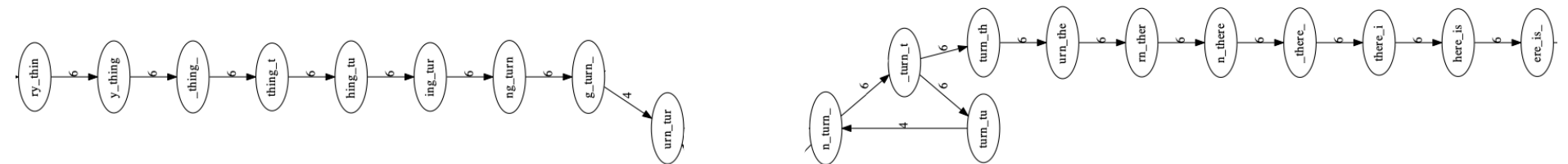
Published: 19 March 2016 **Article history** ▼

Layout – Bubble Collapsing Example

- Overlap graphs may contain **redundant edges**
 - Transitive edges that can be removed without losing the connectivity information of the graph
 - After the transitive reduction:

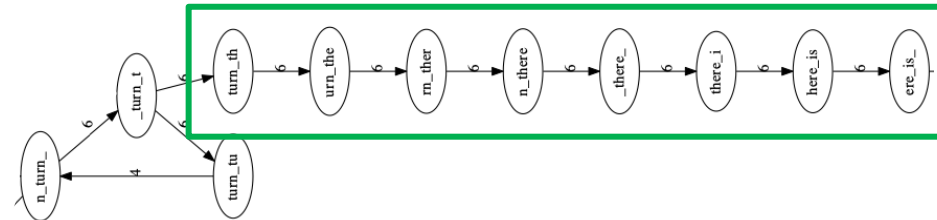
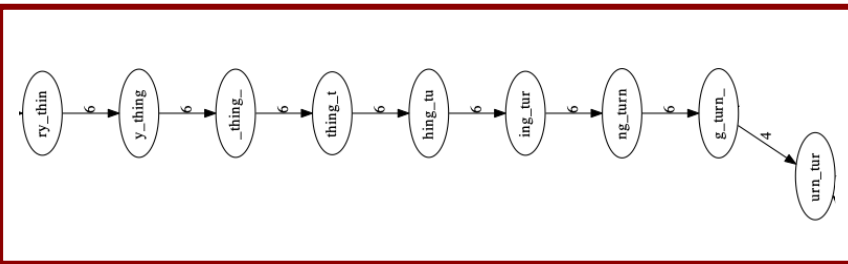


- Bubble Collapsing

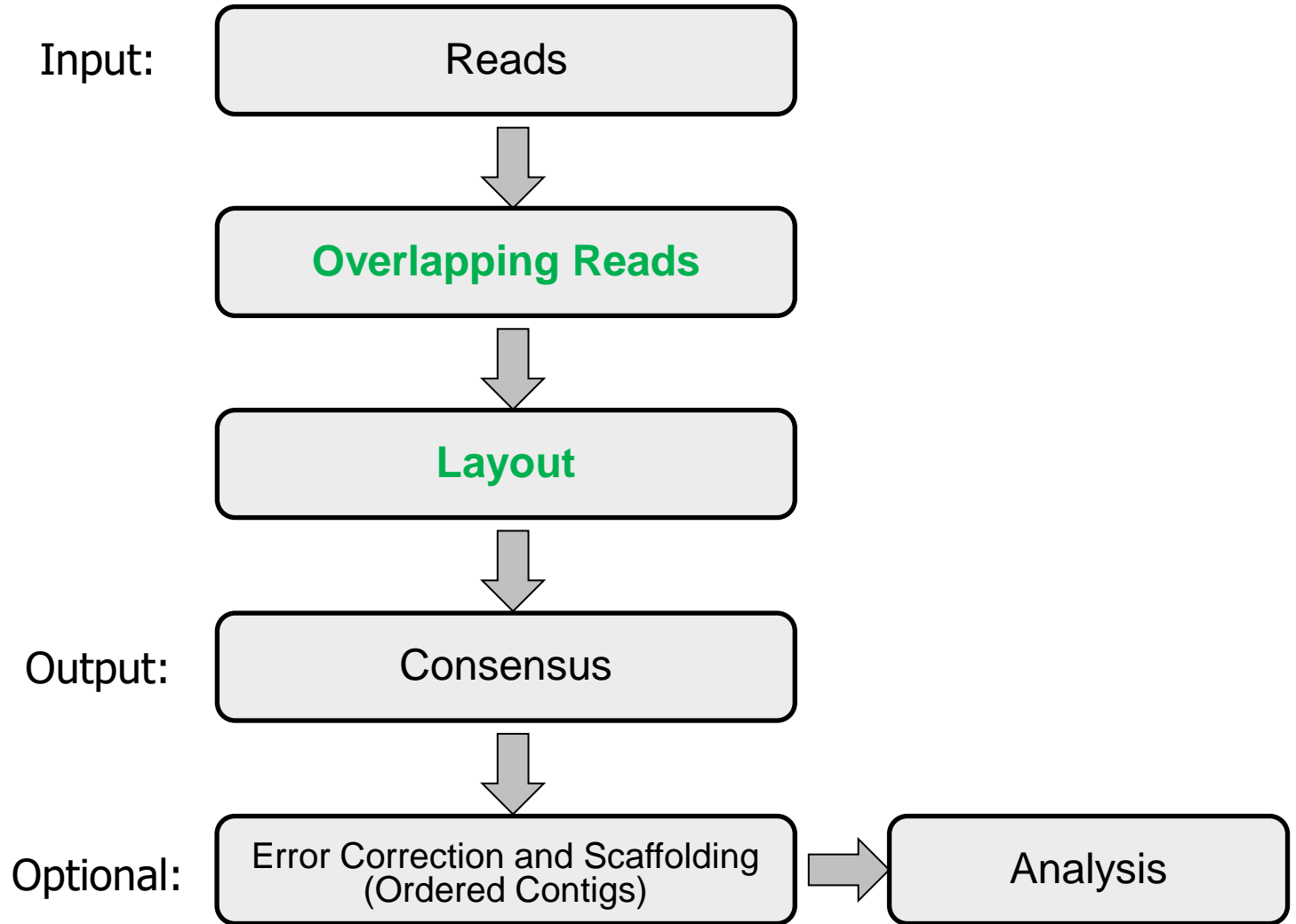


Spelling out the Contigs

- Take all nodes with unambiguous branches (e.g., single branch, leading no cycles)
- “Spell out” the contig by following the unambiguous branches



A Common Assembly Pipeline



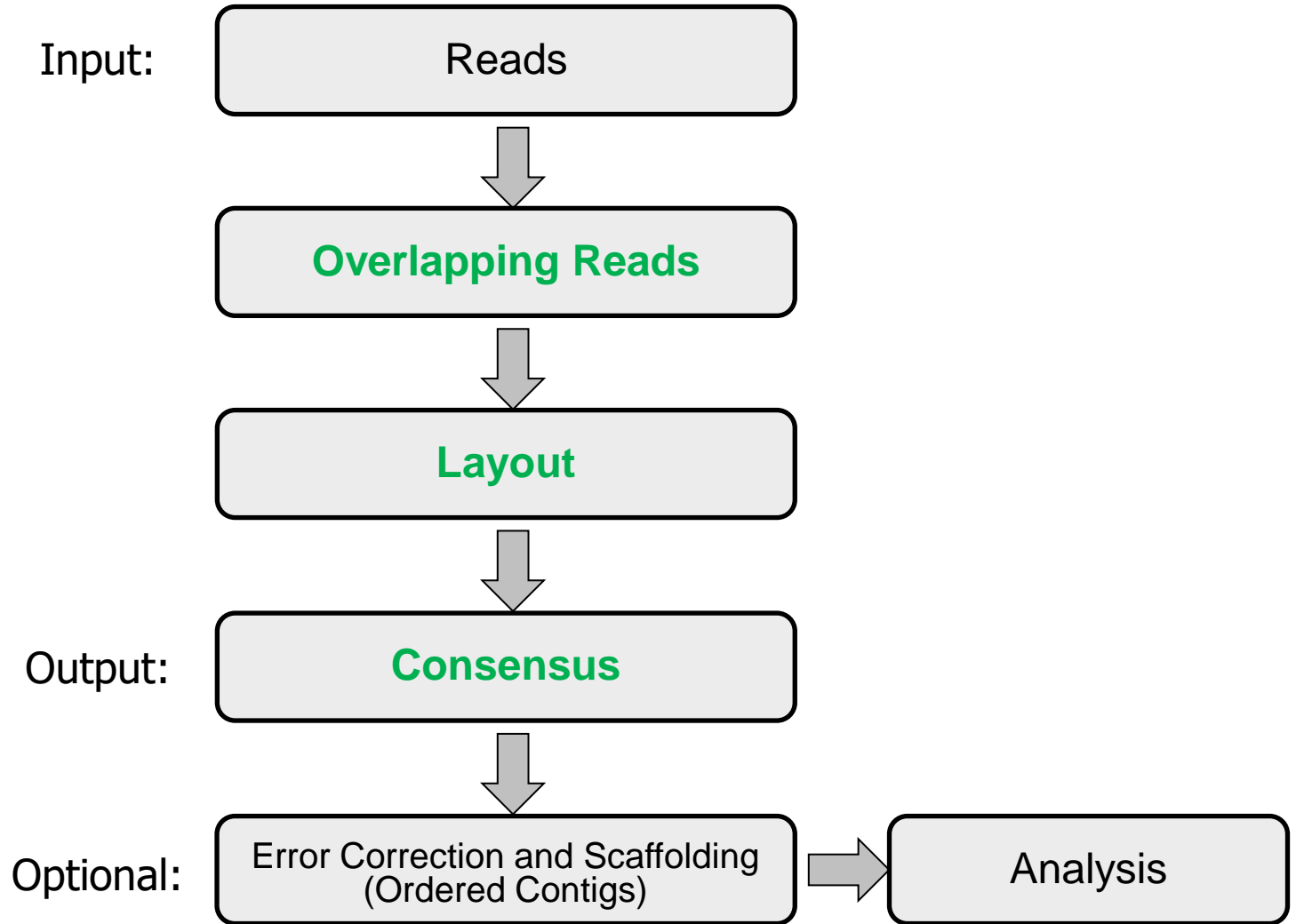
Consensus of Overlapping Reads

- Layout the overlaps of reads from the overlap graph
- Take the consensus at each base to generate contigs

```
ATTGACCTAACCTTTACCT
| | | | | | | | | | | |
TGACCTAATTTTACCT
| | | | | | | | | |
CCTAATTTTAGCTTTAGC
| | | | | | | | | |
TTTACCTTTAGATTGA
| | | | | | | | | |
TACCTTTAGATTGAGGACGACG
| | | | | | | | | |
TAGTTTGAGGACGACGCCAGGAC
ATTGACCTAATTTTACCTTTAGATTGAGGACGACGCCAGGAC
```

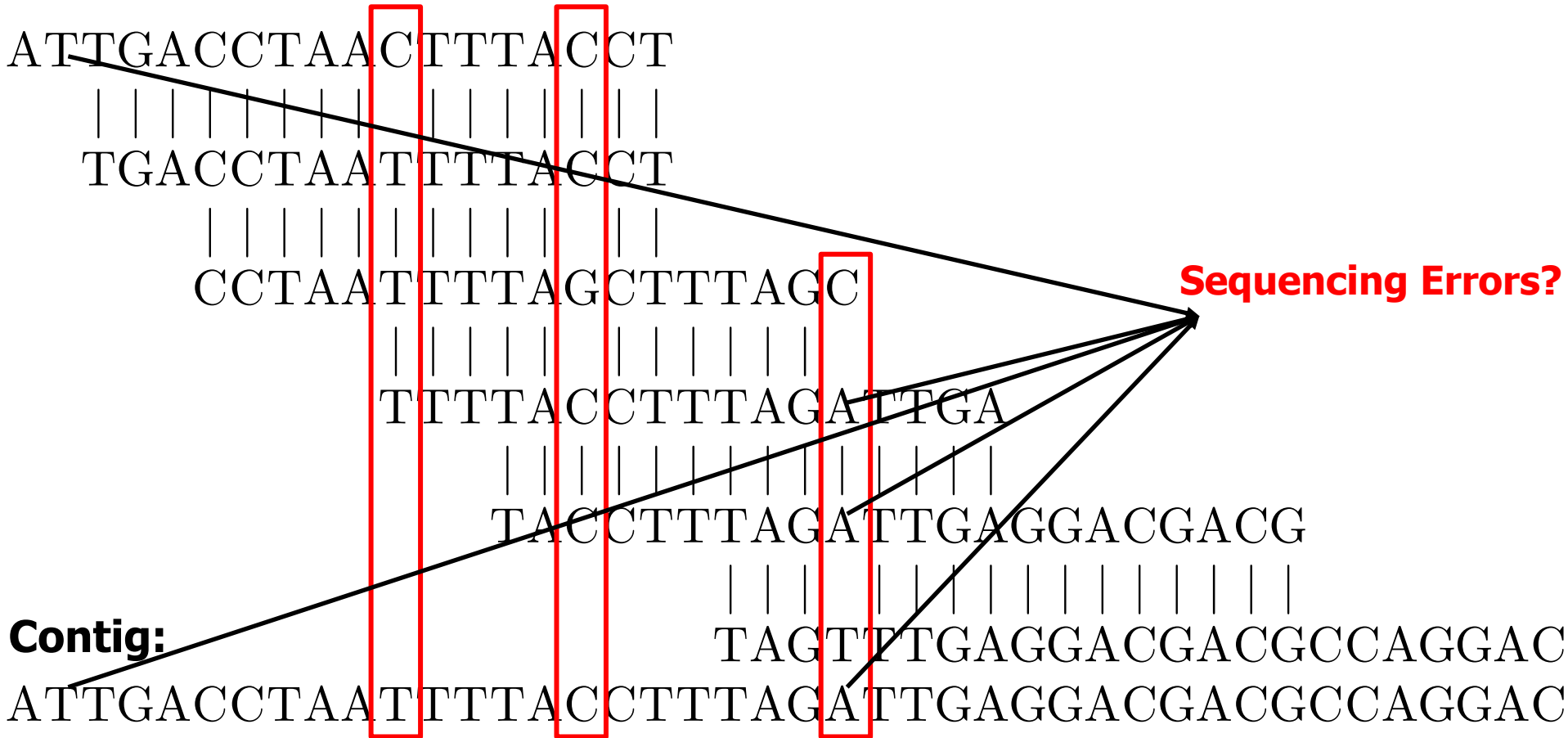
Contig:

A Common Assembly Pipeline



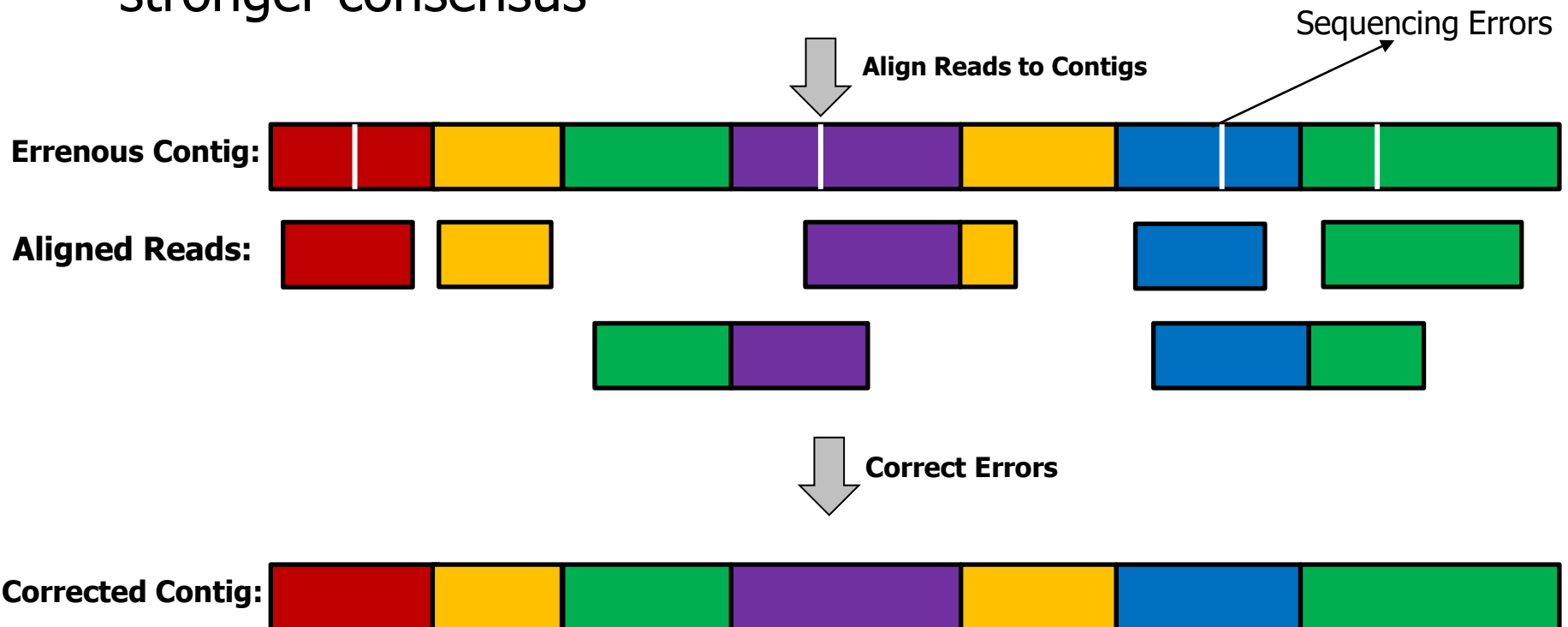
Consensus of Overlapping Reads

- Take the consensus at each base to generate contigs



Assembly Polishing (Error Correction)

- Sequencing errors on reads may propagate to contigs
 - Leading to inaccurate analysis on the assembly we just generated
- Idea: Align reads back to contigs again to generate a stronger consensus



A Reading on Assembly Polishing

- Firtina et al., "[Apollo: A Sequencing-Technology-Independent, Scalable, and Accurate Assembly Polishing Algorithm](#)," *Bioinformatics*, June 2020.

Apollo: a sequencing-technology-independent, scalable and accurate assembly polishing algorithm

FREE

Can Firtina, Jeremie S Kim, Mohammed Alser, Damla Senol Cali, A Ercument Cicek, Can Alkan ✉, Onur Mutlu ✉

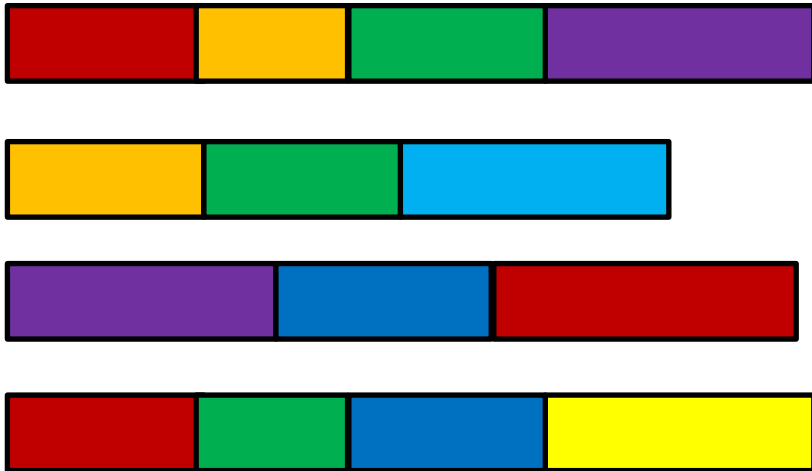
Bioinformatics, Volume 36, Issue 12, 15 June 2020, Pages 3669–3679,
<https://doi.org/10.1093/bioinformatics/btaa179>

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Scaffolding – Ordering the Contigs

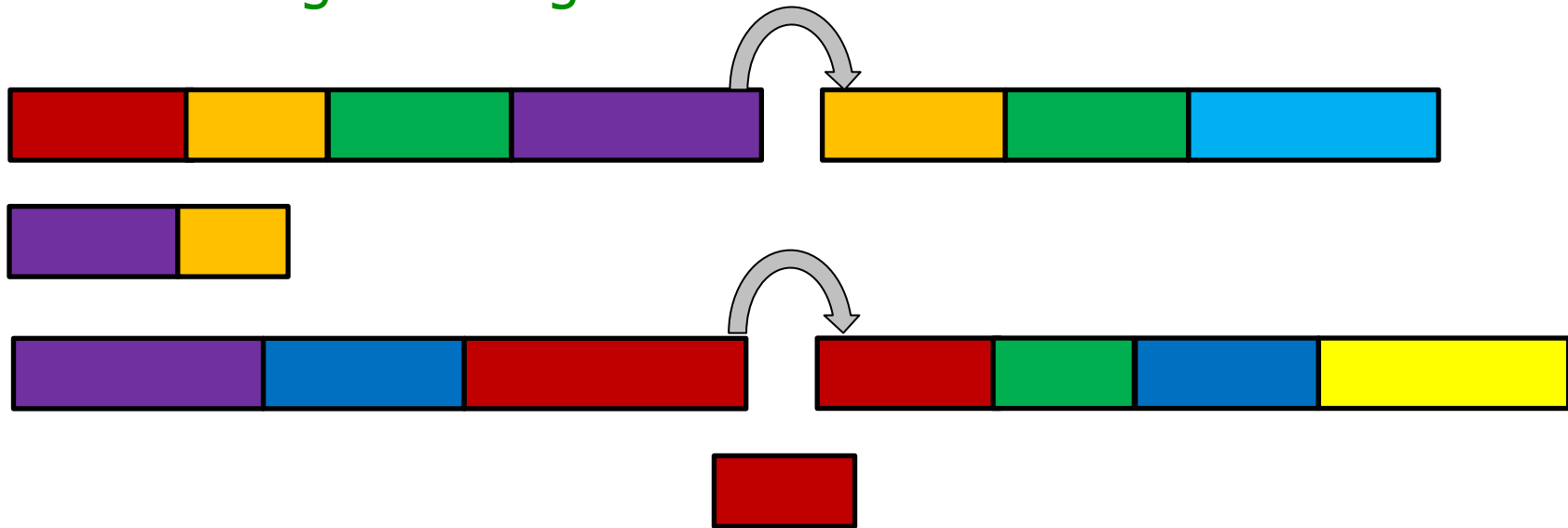
- Contigs are usually **not ordered**
- A **gapless** chromosome may potentially be represented by several **gapped contigs**
 - What is **the relative order of contigs** to represent the genome correctly?

Unordered Contigs:



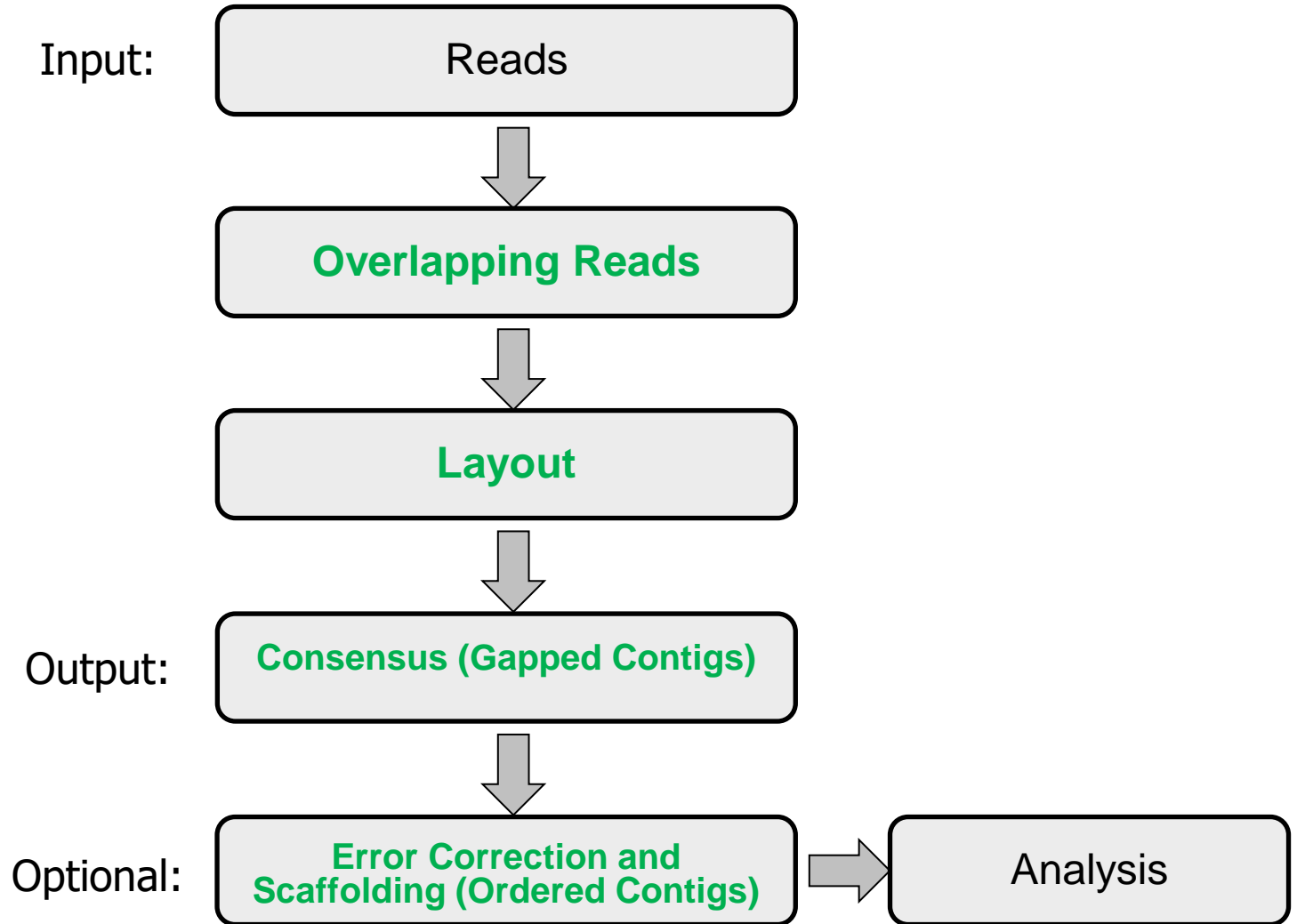
Scaffolding – Ordering the Contigs (cont'd)

- Overlap parts of reads to contigs to find the **pairwise ordering of contigs**



- Ultra long reads, paired-end reads, optical mapping usually help scaffolding
 - These are good keywords to check if you are curious

A Common Assembly Pipeline



What Makes a Good Assembly?

■ **Accurate**

- Should be resolved from **errors** as much as possible
- Solutions:
 - Long and accurate reads (e.g., PacBio HiFi reads)
 - Error correction tools
 - Accurate assemblers

■ **Contiguous**

- **Gaps**: Missing information on assembly
- Solutions:
 - Long and accurate reads
 - Accurate assemblers
 - We need better tools to resolve repeats in overlap graphs

- Tools to generate overlaps: Minimap2, Canu
- Tools for assembly: Miniasm, mdbg, Canu, Hifiasm, Flye
- Tools to assess the assembly quality: QUAST and the MUMmer package

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Lecture 10: Genome Assembly

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